AMENDMENTS TO THE SPECIFICATION

Please amend paragraph **[0016]**, as shown below:

[0016] The present invention also provides isolated porcine adenovirus sequences essential for encapsidation that comprise a nucleotide sequence selected from the group consisting of:

Motif I represented by X_IAAATTY$_I$, wherein X_I is selected from the group consisting of G, GG, CGG, GCGG, and GGCGG, and wherein Y_I is selected from the group consisting of CCCGCACA, CCCGCAC, CCCGCA, CCCGC, CCCG, CCC, CC and C (SEQ ID NOS: 1, 2, 91, 103-139);

Motif II represented by X_{II}ATTTTY$_{II}$, wherein X_{II} is selected from the group consisting of G, GG, GGG, CGGG, and GCGGG, and wherein Y_{II} is selected from the group consisting of GTGCCCTCT, GTGCCCTC, GTGCCCT, GTGCCC, GTGCC, GTGC, GTG, GT and G (SEQ ID NOS: 3, 4, 95, 140-181);

Motif III represented by X_{III}TATTY$_{III}$,wherein X_{III} is selected from the group consisting of G, GG, CGG, CCGG, and CCCGG, and wherein Y_{III} is selected from the group consisting of CCCCACCTG, CCCCACCT, CCCCACC, CCCCAC, CCCCA, CCCC, CCC, CC, and C (SEQ ID NOS: 5, 6, 97, 182-223);

Motif IV represented by X_{IV}TATTTTTTY$_{IV}$, wherein X_{IV} is selected from the group consisting of G, TG, GTG, GGTG, and GGGTG, and wherein Y_{IV} is selected from the group consisting of CCCCTCA, CCCCTC, CCCCT, CCCC, CCC, CC, and C SEQ ID NOS: 7, 8, 100, 224-255);

Motif V represented by X_VTATATAY$_V$, wherein X_V is selected from the group consisting of G, TG, GTG, AGTG, and CAGTG, and wherein Y_V is selected from the group consisting of GTCCGCGC, GTCCGCG, GTCCGC, GTCCG, GTCC, GTC, GT and G (SEQ ID NOS: 9, 10, 101, 256-292); and

Motif VI represented by X_{VI}TTTTY$_{VI}$, wherein X_{VI} is selected from the group consisting of G, AG, GAG, AGAG, and TAGAG, wherein Y_{VI} is selected from the group consisting of CTCTCAGCG, CTCTCAGC, CTCTCAG, CTCTCA, CTCTC, CTCT, CTC, CT and C (SEQ ID NOS: 11, 12, 99, 102, 293-333).

Please amend paragraph **[0017]**, as shown below:

[0017] The present invention further provides isolated porcine adenovirus sequences essential for encapsidation that comprise a nucleotide sequence selected from the group consisting of:

Motif 1 represented by X_1TATTTTTY_1, wherein X_1 is selected from the group consisting of G, GG, TGG, and CTGG, and wherein Y_1 is selected from the group consisting of C, CC, CCA, and CCAC (SEQ ID NOS: 13, 334-348);

Motif 2 represented by X_2ATATTY$_2$, wherein X_2 is selected from the group consisting of G, TG, and GTG, and wherein Y_2 is selected from the group consisting of G and GG (SEQ ID NOS: 14, 349-353);

Motif 3 represented by X_3TTTAY$_3$, wherein X_3 is selected from the group consisting of C and CC, and wherein Y_3 is selected from the group consisting of C, CC, CCT, CCTG, CCTGG, and CCTGGG (SEQ ID NOS: 15, 354-364);

Motif 4 represented by X_4AATTTTAY$_4$, wherein X_4 is selected from the group consisting of C, TC, and CTC, and wherein Y_4 is selected from the group consisting of C, CC, CCA, and CCAC (SEQ ID NOS: 16, 365-375);

Motif 5 represented by X_5ATTTTTY$_5$, wherein X_5 is selected from the group consisting of G, CG, TCG, GTCG, and GGTCG, and wherein Y_5 is selected from the group consisting of C, CC, CCA, and CCAC (SEQ ID NOS: 17, 376-394); and

Motif 6 represented by X_6TATTTATTY$_6$, wherein X_6 is selected from the group consisting of C, CC, and CCC, and wherein Y_6 is selected from the group consisting of C, CT, CTG, CTGC, CTGCG, CTGCGC, and CTGCGCG (SEQ ID NOS: 18, 20, 395-413).

Please amend paragraph no. **[0018]**, as follows:

[0018] In some examples, the porcine adenovirus sequence essential for encapsidation is a porcine adenovirus 3 sequence. In some examples, the porcine adenovirus sequence essential for encapsidation of porcine adenovirus type-3 is located between about nucleotide position 212 and about nucleotide position 531 at the left end of the genome. In other examples, the porcine

adenovirus sequence essential for encapsidation is a porcine adenovirus 5 sequence. In other examples, an isolated porcine adenovirus sequence essential for encapsidation comprises a nucleotide sequence selected from the group consisting of:
CGGAAATTCCCGCACA (SEQ ID NO: 1); GGCGGAAATTCCCGCACA (SEQ ID NO: 2); GGGATTTTGTGCCCTCT (SEQ ID NO: 3); GCGGGATTTTGTGCCCTCT (SEQ ID NO: 4); CGGTATTCCCCACCTG (SEQ ID NO: 5); CCCGGTATTCCCCACCTG (SEQ ID NO: 6); GTGTATTTTTTCCCCTCA (SEQ ID NO: 7); GGGTGTATTTTTTCCCCTCA (SEQ ID NO: 8); GTGTATATAGTCCGCGC (SEQ ID NO: 9); CAGTGTATATAGTCCGCGC (SEQ ID NO: 10); GAGTTTTCTCTCAGCG (SEQ ID NO: 11); and TAGAGTTTTCTCTCAGCG (SEQ ID NO: 12).

Please amend paragraph no. **[0019]**, as follows:

[0019] In other examples, an isolated porcine adenovirus sequence essential for encapsidation comprises a nucleotide sequence selected from the group consisting of:
CTGGTATTTTCCAC (SEQ ID NO: 13); GTGATATTGG (SEQ ID NO: 14); CCTTTACCTGGG (SEQ ID NO: 15); CTCAATTTTACCAC (SEQ ID NO: 16); GGTCGATTTTTCCAC (SEQ ID NO: 17); and CCTATTTATTCTGCGCG (SEQ ID NO: 18).

Please amend paragraph no. **[0030]**, as follows:

[0030] Figures 1A-1B show the nucleotide sequence of PAV3 terminus. Numbers indicate the nucleotide position relative to the left terminus. Inverted terminal repeat(ITR) is shown by italic type. The cap site and ATG codon for E1A gene are shown in italic bold face. AT-rich motifs were underlined. Fig. 1A shows the nucleotide sequence of PAV3 left terminus (SEQ ID NO: 86). Fig. 1B shows the nucleotide sequence of PAV3 right terminus (SEQ ID NO: 87).

Please amend paragraph no. **[0041]**, as follows:

[0041] Figure 12 shows a sequence alignment of packaging motifs of PAV3. Numbers indicate the position of AT sequences in the motifs relative to the left terminus of PAV3 genome (SEQ ID NOs: 1, 3, 5, 7, 9, 11).

Please amend paragraph no. **[0042]**, as follows:

[0042] Figures 13A-13B. PAV-3 E1A transcriptional control region. (Fig. 13A). Schematic diagram of E1A transcriptional control region of PAV-3 and mutant viruses. The inverted terminal repeat (ITR) and potential cis-acting packaging domains are represented with hatched and open boxes, respectively. The E1A cap site and the translation start site (ATG) are indicated by the stippled circle and arrow, respectively. The individual deletion mutant names are given on the left. The deleted sequences are indicated with the bold lines. Nucleotide numbers relative to the left terminus of the genome designate the last base pair present on either side of deletions. (Fig. 13B). Nucleotide sequences (SEQ ID NO: 88) of the functionally two-faced regulatory element. Arrows designate repeated constituents located within regulatory element. Potential cis-acting packaging motifs were underlined

Please amend paragraph no. **[0049]**, as follows:

[0049] Figure 20. Nucleotide sequence (SEQ ID NO: 89) of cis-acting packaging domain of PAV-3. Numbers indicate the nucleotide position relative to the left terminus of PAV-3 genome. The sequences analyzed in this study were in bold face and underlined. Packaging motifs were indicated with I, II, III, IV, V, and V1.

Please amend paragraph no. **[0050]**, as follows:

[0050] Figures 21A-21B. (SEQ ID NOs: 90-97) Analysis of viral mutants constructed in the background of Pav3-151/383 (1), Pav3-312/531 (2), and Pav3-382/531 (3). (A) The top of the

figure shows the sequences analyzed. Figure 21A(1) shows data from PAV3 packaging motif I. Figure 21A(2) shows data for PAV3 packaging motif I and II. Figure 21A(3) shows data for motif I, II, and III. The targeted sequences in this study were underlined. The SpeI linker replacing the targeted sequences was pointed with an arrow. The individual deletion mutant names are given on the left. The dotted lines indicate the sequences deleted are indicated by dotted line. Mutant virus yields (Yield) are expressed as the fold reduction in yield relative to that of wild-type virus. Mutant virus packaging efficiency (COINF) is expressed as the fold reduction in packaged mutant DNA relative to the packaged coinfecting wild type DNA. The data were normalized to the amount of each viral DNA (mutant and wild-type) present in total nuclear DNA. No viable virus (NV). (B) Southern hybridization analysis of viral DNA represented either in total DNA or in virion particles isolated from VIDO R1 cells coinfected with wild-type and the mutant viruses. Total nuclear DNA and virion DNA were digested with SpeI and KpnI and subsequently subjected to Southern hybridization analysis using PAV-3 left end fragment between nt 531 and 844 as a ^{32}P-labeled probe. The corresponding wild-type (WT) and mutant (MU) left end DNA fragments are indicated. The mutant viruses tested were Pav3-PL1 (lane 1), Pav3-PM3 (lane 2), Pav3-PA12 (lane 3), Pav3-PA3 (lane 4), Pav3-PL3 (lane 5), Pav3-PRl (lane 6), Pav3-PR3 (lane 7), Pav3-PM5 (lane 8).

Please amend paragraph no. **[0051]**, as follows:

[0051] Figures 22A-22B. (SEQ ID NOs: 98-102) Analysis of viral mutants constructed in the background of Pav3-151/383. (A) The legend is as described for Figure 21A. Data are shown for motifs PAV packaging motifs IV, V, and VI. (B) Southern hybridization analysis of nuclear and virion DNA isolated from VIDO R1 cells coinfected with wild-type and individual mutant viruses. Southern hybridization analysis of total nuclear DNA and virion DNA was performed as described in the legend to Figure 21B. The mutant viruses tested were Pav3-PM7 (lane 1), Pav3-PM9 (lane 2), Pav3-PM112 (lane 3), Pav3-PA9 (lane 4), Pav3-PA112 (lane 5), Pav3-PL9 (lane 6), Pav3-PL11 (lane 7), Pav3-PR9 (lane 8), Pav3-PR112 (lane 9).

Please amend paragraph no. **[0078]**, as follows:

[0078] The complete genome sequence of human adenovirus 5 is disclosed in GenBank accession number M73260 and the complete genome sequence of human adenovirus 2 is disclosed in GenBank accession number J01917, the sequences of which are incorporated herein by reference. The cis-acting packaging domain of human adenovirus -5 (HAV-5) is located in the left end 380 bp (Hearing, 1987, *J. Virol.* 61:2555-2558). It contains at least seven functionally redundant "A-repeat" domains, four of which (A1, AII, AV and AVI) are most relevant (Grable, 1990, *J. Virol.* 64:2047-2056). Mutational analysis of A-repeat consensus sequence (5'-TTTGN_8CG-3') (SEQ ID NO: 19) suggested that two elements 5'-TTTG-3' and 5'-CG-3' of the sequence, as well as the spacing (N_8) are critical for maximum packaging capacity (Schmid et al., 1997, *J. Virol.*. 71:3375-3384). In addition to cis-acting sequences, a number of viral and / or cellular proteins are thought to be involved in adenovirus DNA packaging. Schmid and Hearing have detected some cellular proteins binding to the packaging sequences (Schmid, 1998, *J. Virol.* 72:6339-6347). Among viral proteins, the 52 / 55-kDa and IVa2 proteins have been shown to date to be required for viral DNA packaging (Zhang et al., 2000, *J. Virol.* 74:2687-2690; Gustin et al., 1998, *J. Virol.*72:7860-7870). Interaction of IVa2 with the different components of the DNA packaging machinery has been shown to be serotype specific (Zheng et al., *J. Virol.* 75:10446-10459).

Please amend paragraph no. **[0079]**, as follows:

[0079] The present invention relates to the identification and characterization of PAV regions essential for encapsidation, also referred to herein as packaging domains. Based on the identification of cis-acting packaging domain of human adenovirus 5 (HAV5), 5' TTTGN[[8]]$_8$CG-3' (SEQ ID NO: 19) (Schmid et al. 1997, *J. Virol.* 71:3375-3384) the PAV3 genome was searched to identify putative packaging domains. The packaging domain of porcine adenovirus type-3 is located between about nucleotide position 212 and about 531 at the left end of the genome. No regions were found that showed perfect homology with the consensus packaging domain of HAV5. As shown in the examples, a series of mutations were made in PAV-3 genome in order to determine the regions essential for PAV encapsidation. Data shown herein in the examples demonstrate that

there are at least six AT-rich motifs which can provide the packaging ability to PAV3. Table 1 provides a listing of the regions.

Please amend paragraph no. **[0080]**, as follows:

Table 1

[0080] Alignment of Packaging sequences of PAV3 (numbering refers to the location of the A/T rich regions within the PAV-3 genome)

233-237		CGG	AAATT	CCCGCACA (SEQ ID NO: 1)
264-268		GGG	ATTTT	GTGCCCTCT (SEQ ID NO: 3)
334-337		CGG	TATT	CCCCACCTG (SEQ ID NO: 5)
431-438		GTG	TATTTTTT	CCCCTCA (SEQ ID NO: 7)
449-454		GTG	TATATA	GTCCGCGC (SEQ ID NO: 9)
505-508		GAG	TTTT	CTCTCAGCG (SEQ ID NO: 11)
233-237	GG	CGG	AAATT	CCCGCACA (SEQ ID NO: 2)
264-268	GC	GGG	ATTTT	GTGCCCTCT (SEQ ID NO: 4)
334-337	CC	CGG	TATT	CCCCACCTG (SEQ ID NO: 6)
431-438	GG	GTG	TATTTTTT	CCCCTCA (SEQ ID NO: 8)
449-454	CA	GTG	TATATA	GTCCGCGC (SEQ ID NO: 10)
505-508	TA	GAG	TTTT	CTCTCAGCG (SEQ ID NO:12)

Please amend paragraph no. **[0082]**, as follows:

Table 2

[0082] Alignment of expected packaging sequences of PAV5 (numbering refers to the location of the A/T rich regions within the PAV-5 genome)

187-192 (SEQ ID NO: 13)	CTGG	TATTTT	CCAC

207-211 (SEQ ID NO: 14)	GTG	ATATT	GG
217-220 (SEQ ID NO: 15)	CC	TTTA	CCTGGG
272-277 (SEQ ID NO: 16)	CTC	AATTTTA	CCAC
321-326 (SEQ ID NO: 17)	GGTCG	ATTTTT	CCAC
349-356 (SEQ ID NO: 20)	CCC	TATTTATT	CTGCGCG

Please amend paragraph no. **[0084]**, as follows:

[0084] The present invention also provides isolated porcine adenovirus sequences essential for encapsidation that comprise a nucleotide sequence selected from the group consisting of:

Motif I represented by X_IAAATTY$_I$, wherein X_I is selected from the group consisting of G, GG, CGG, GCGG, and GGCGG, and wherein Y_I is selected from the group consisting of CCCGCACA, CCCGCAC, CCCGCA, CCCGC, CCCG, CCC, CC and C (SEQ ID NOS: 1, 2, 91, 103-139);

Motif II represented by X_{II}ATTTTY$_{II}$, wherein X_{II} is selected from the group consisting of G, GG, GGG, CGGG, and GCGGG, and wherein Y_{II} is selected from the group consisting of GTGCCCTCT, GTGCCCTC, GTGCCCT, GTGCCC, GTGCC, GTGC, GTG, GT and G (SEQ ID NOS: 3, 4, 95, 140-181);

Motif III represented by X_{III}TATTY$_{III}$,wherein X_{III} is selected from the group consisting of G, GG, CGG, CCGG, and CCCGG, and wherein Y_{III} is selected from the group consisting of CCCCACCTG, CCCCACCT, CCCCACC, CCCCAC, CCCCA, CCCC, CCC, CC, and C (SEQ ID NOS: 5, 6, 97, 182-223);

Motif IV represented by X_{IV}TATTTTTTY$_{IV}$, wherein X_{IV} is selected from the group consisting of G, TG, GTG, GGTG, and GGGTG, and wherein Y_{IV} is selected from the group consisting of CCCCTCA, CCCCTC, CCCCT, CCCC, CCC, CC, and C (SEQ IDS NOS: 7, 8, 100, 224-255);

Motif V represented by X_VTATATAY$_V$, wherein X_V is selected from the group consisting of G, TG, GTG, AGTG, and CAGTG, and wherein Y_V is selected from the group consisting of

GTCCGCGC, GTCCGCG, GTCCGC, GTCCG, GTCC, GTC, GT and G (SEQ ID NOS: 9, 10, 101, 256-292); and

Motif VI represented by X_{VI}TTTTY$_{VI}$, wherein X_{VI} is selected from the group consisting of G, AG, GAG, AGAG, and TAGAG, wherein Y_{VI} is selected from the group consisting of CTCTCAGCG, CTCTCAGC, CTCTCAG, CTCTCA, CTCTC, CTCT, CTC, CT and C (SEQ ID NOS: 11, 12, 99, 102, 293-333).

Please amend paragraph no. **[0085]**, as follows:

[0085] The present invention further provides isolated porcine adenovirus sequences essential for encapsidation that comprise a nucleotide sequence selected from the group consisting of:

Motif 1 represented by X_1TATTTTY$_1$, wherein X_1 is selected from the group consisting of G, GG, TGG, and CTGG, and wherein Y_1 is selected from the group consisting of C, CC, CCA, and CCAC (SEQ ID NOS: 13, 334-348);

Motif 2 represented by X_2ATATTY$_2$, wherein X_2 is selected from the group consisting of G, TG, and GTG, and wherein Y_2 is selected from the group consisting of G and GG (SEQ ID NOS: 14, 349-353);

Motif 3 represented by X_3TTTAY$_3$, wherein X_3 is selected from the group consisting of C and CC, and wherein Y_3 is selected from the group consisting of C, CC, CCT, CCTG, CCTGG, and CCTGGG (SEQ ID NOS: 15, 354-364);

Motif 4 represented by X_4AATTTTAY$_4$, wherein X_4 is selected from the group consisting of C, TC, and CTC, and wherein Y_4 is selected from the group consisting of C, CC, CCA, and CCAC (SEQ ID NOS: 16, 365-375);

Motif 5 represented by X_5ATTTTTY$_5$, wherein X_5 is selected from the group consisting of G, CG, TCG, GTCG, and GGTCG, and wherein Y_5 is selected from the group consisting of C, CC, CCA, and CCAC (SEQ ID NOS: 17, 376-394); and

Motif 6 represented by X_6TATTTATTY$_6$, wherein X_6 is selected from the group consisting of C, CC, and CCC, and wherein Y_6 is selected from the group consisting of C, CT, CTG, CTGC, CTGCG, CTGCGC, and CTGCGCG (SEQ ID NOS: 18, 20, 395-413).

Please amend paragraph no. **[0086]**, as follows:

[0086] The present invention encompasses vectors, including adenovirus vectors, comprising a porcine adenovirus sequence(s) essential for encapsidation. At least one porcine adenovirus sequence essential for encapsidation is necessary for inserting adenovirus DNA into adenovirus capsids. In some examples, a vector, such as for example, an adenovirus vector comprises at least one porcine adenovirus sequence essential for encapsidation that comprises a nucleotide sequence selected from the group consisting of AAATT; ATTTT; TATT; TATTTTTT; TATATA; TTTT; TATTTT; ATATT; TTTA; AATTTTA; ATTTTT; and TATTTATT. In other examples, a vector, such as for example, an adenovirus vector, comprises at least one porcine adenovirus sequence essential for encapsidation that comprises a nucleotide sequence selected from the group consisting of:

Motif I represented by X_IAAATTY$_I$, wherein X_I is selected from the group consisting of G, GG, CGG, GCGG, and GGCGG, and wherein Y_I is selected from the group consisting of CCCGCACA, CCCGCAC, CCCGCA, CCCGC, CCCG, CCC, CC and C (SEQ ID NOS: 1, 2, 91, 103-139);

Motif II represented by X_{II}ATTTTY$_{II}$, wherein X_{II} is selected from the group consisting of G, GG, GGG, CGGG, and GCGGG, and wherein Y_{II} is selected from the group consisting of GTGCCCTCT, GTGCCCTC, GTGCCCT, GTGCCC, GTGCC, GTGC, GTG, GT and G (SEQ ID NOS: 3, 4, 95, 140-181);

Motif III represented by X_{III}TATTY$_{III}$,wherein X_{III} is selected from the group consisting of G, GG, CGG, CCGG, and CCCGG, and wherein Y_{III} is selected from the group consisting of CCCCACCTG, CCCCACCT, CCCCACC, CCCCAC, CCCCA, CCCC, CCC, CC, and C (SEQ ID NOS: 5, 6, 97, 182-223);

Motif IV represented by X_{IV}TATTTTTTY$_{IV}$, wherein X_{IV} is selected from the group consisting of G, TG, GTG, GGTG, and GGGTG, and wherein Y_{IV} is selected from the group consisting of CCCCTCA, CCCCTC, CCCCT, CCCC, CCC, CC, and C (SEQ ID NOS: 7, 8, 100, 224-255);

Motif V represented by $X_VTATATAY_V$, wherein X_V is selected from the group consisting of G, TG, GTG, AGTG, and CAGTG, and wherein Y_V is selected from the group consisting of GTCCGCGC, GTCCGCG, GTCCGC, GTCCG, GTCC, GTC, GT and G (SEQ ID NOS: 9, 10, 101, 256-292); and

Motif VI represented by $X_{VI}TTTTY_{VI}$, wherein X_{VI} is selected from the group consisting of G, AG, GAG, AGAG, and TAGAG, wherein Y_{VI} is selected from the group consisting of CTCTCAGCG, CTCTCAGC, CTCTCAG, CTCTCA, CTCTC, CTCT, CTC, CT and C (SEQ ID NOS: 11, 12, 99, 102, 293-333).

Please amend paragraph no. **[0087]**, as follows:

[0087] In further examples, a vector, such as for example, an adenovirus vector, comprises at least one porcine adenovirus sequence essential for encapsidation that comprises a nucleotide sequence selected from the group consisting of:

Motif 1 represented by $X_1TATTTTY_1$, wherein X_1 is selected from the group consisting of G, GG, TGG, and CTGG, and wherein Y_1 is selected from the group consisting of C, CC, CCA, and CCAC (SEQ ID NOS: 13, 334-348);

Motif 2 represented by $X_2ATATTY_2$, wherein X_2 is selected from the group consisting of G, TG, and GTG, and wherein Y_2 is selected from the group consisting of G and GG (SEQ ID NOS: 14, 349-353);

Motif 3 represented by X_3TTTAY_3, wherein X_3 is selected from the group consisting of C and CC, and wherein Y_3 is selected from the group consisting of C, CC, CCT, CCTG, CCTGG, and CCTGGG (SEQ ID NOS: 15, 354-364);

Motif 4 represented by $X_4AATTTTAY_4$, wherein X_4 is selected from the group consisting of C, TC, and CTC, and wherein Y_4 is selected from the group consisting of C, CC, CCA, and CCAC (SEQ ID NOS: 16, 365-375);

Motif 5 represented by $X_5ATTTTTY_5$, wherein X_5 is selected from the group consisting of G, CG, TCG, GTCG, and GGTCG, and wherein Y_5 is selected from the group consisting of C, CC, CCA, and CCAC (SEQ ID NOS: 17, 376-394); and

Motif 6 represented by X_6TATTTATTY$_6$, wherein X_6 is selected from the group consisting of C, CC, and CCC, and wherein Y_6 is selected from the group consisting of C, CT, CTG, CTGC, CTGCG, CTGCGC, and CTGCGCG (SEQ ID NOS: 18, 20, 395-413).

Please amend paragraph no. **[0168]**, as follows:

Table 3.

[0168] Primers used in this study. The restriction endonuclease cleavage sites are underlined. Numbers indicate the nucleotide position relative to the left terminus of PAV3 genome. PAV3 nucleotide sequences are indicated in boldface type.

P1: 5'-CGT CTT CAA GGA TCC TTA-3' (sense, BamH I)
(SEQ ID NO: 21)
P2: 5'-**CGC GCT GAT ATC CTC CTC-3'** (anti sense, EcoR V, 827-844)
(SEQ ID NO: 22)

P3: 5'-CCG CAA TTG **GTC ATC ACA CGT CAT TTT C**-3'(antisense, Mfe I, 133-151)
(SEQ ID NO: 23)
P4: 5'-CCG CAA TTG **GGG GCG GGG CCG AGC GGC**-3' (sense, Mfe I, 213-230)
(SEQ ID NO: 24)

P5: 5'-CCG CAA TTG **GCG GAG GAC CGC CCC AGG**-3'(antisense, Mfe I, 195-212)
(SEQ ID NO: 25)
P6: 5'-CCG CAA TTG **ATA CCG CGG GAT TTT GT**-3' (sense, Mfe I, 255-271)
(SEQ ID NO: 26)

P7: 5'-CCG CAA TTG **CTC CAC CTG TGC GGG AAT**-3' (antisense, Mfe I, 235-252)
(SEQ ID NO: 27)
P8: 5'-CCG CAA TTG **CAC CAC ACG TCC GCG G**-3' (sense, Mfe I, 313-328)
(SEQ ID NO: 28)

P9: 5'-CCG CAA TTG **CGG AAG TGC CAC ACC GGA**-3' (antisense, Mfe I, 295-312)
(SEQ ID NO: 29)
P10: 5'-CCG CAA TTG **TCG CGC TGA GAG GTC CGC G**-3'(sense, Mfe I, 383-401)
(SEQ ID NO: 30)

P11: 5'-CCG CAA TTG **AGG ACA CCC CGC TCA GGT**-3' (antisense, Mfe I, 365-382)
(SEQ ID NO: 31)

P12: 5'-CCG CAA TTG **TTT TTT CCC CTC AGT GTA TA**-3'(sense, Mfe I, 433-452)
(SEQ ID NO: 32)

P13: 5'-CCG CAA TTG **TAC ACC CAC ACA CGT CAT**-3' (antisense, Mfe I, 415-432)
(SEQ ID NO: 33)
P14: 5'-CCG CAA TTG **TAT ATA GTC CGC GCA**-3' (sense, Mfe I, 449-463)
(SEQ ID NO: 34)

P15: 5'-CCG CAA TTG **ACT GAG GGG AAA AAA TAC**-3' (antisense, Mfe I, 430-447)
(SEQ ID NO: 35)
P16: 5'-CCG CAA TTG **GTC ACT ACT CTT GAG TCC**-3' (sense, Mfe I, 474-491)
(SEQ ID NO: 36)

P17: 5'-CCG CAA TTG **CGC GGA CTA TAT ACA CTG**-3' (antisense, Mfe I, 444-461)
(SEQ ID NO: 37)
P18: 5'-CCG CAA TTG **GAG TAG AGT TTT CTC TCA**-3' (sense, Mfe I, 497-514)
(SEQ ID NO: 38)

P19: 5'-CCG CAA TTG **CTT CGG ACT CAA GAG TAG**-3' (antisense, Mfe I, 478-495)
(SEQ ID NO: 39)
P20: 5'-CCG CAA TTG **ACA TGG CGA ACA GAC TTC**-3' (sense, Mfe I, 531-548)
(SEQ ID NO: 40)

PR1: 5'-**CCG CCT CCG CGT TAA CGA TTA ACC**-3' (sense, Hpa I, 33838-33861)
(SEQ ID NO: 41)
PR2: 5'-AGC TTT TAA TTA **ACA TCA TC**-3' (antisense, Pac I, 34088-34094)
(SEQ ID NO: 42)

PR3: 5'-CCG CAA TTG **CGC AGG TCG CGG CGG AGC**-3' (antisense, Mfe I, 33894-33911)
(SEQ ID NO: 43)
PR4: 5'-CCG CAA TTG **CCT CGG ACT TTG ACC GT**-3' (sense, Mfe I, 33926-33942)
(SEQ ID NO: 44)

PR5: 5'-CCG CAA TTG **GGC GGG GTC AAA GTC GCA**-3'(antisense, Mfe I, 33908-33926)
(SEQ ID NO: 45)
PR6: 5'-CCG CAA TTG **CCA CGT CAT TTT CCC A**-3' (sense, Mfe I, 33949-33965)
(SEQ ID NO: 46)

PSR32: 5'-CGG CGG GAT CCT TAA TTA A***CA TCA TCA ATA ATA TAC CGC ACA CTT TT***-3' (1-18) (SEQ ID NO: 47)

Please amend paragraph no. **[0194]**, as follows:

[0194] Like HAV (Russell, W. C., 2000, *J. Gen. Virol.* **81**:2573-2604), the E1A and E1B of PAV-3 are transcribed from different promoters (Reddy et al. (1998, *Virus Res.* **58**:97-106). It appears that the regulatory element for E1A overlaps with that for E1B and share some of the common DNA sequences to regulate the transcription by different mechanisms. For adenoviral productive infection, E1A is used to stimulate the cell cycle into S phase (Boulanger et al. (1991, *Biochem. J.* **275**:281-299). This regulation of cell cycle subsequently activates a premature cell death (apoptosis) (Chiou et al., 1997, *J. Virol.* **71**:3515-3525); (Lowe et al., 1993, *Genes Dev.* 7:535-545). In contrast, the proteins encoded by E1B including 19 kDa and 55 kDa can function independently to inhibit apoptosis induced by E1A. (Debbas et al., 1993, *Genes Dev.* **7**:546-554); (Goodrum et al., 1997, T *J. Virol.* **71**:548-561). In addition, E1A and E1B have opposite functions in transactivation of other early promoters. For instance, the E2 late promoter is repressed by E1A (Guilfoyle et al., 1985, *EMBO J.* **4**:707-713), but is induced by E1B 55kDa (Holm et al., 2002, *J. Biol. Chem.* **277**:10427-10434). To manipulate the cells for productive viral infection, it is required that virus expresses the proteins with counteracting functions in a proper proportion. Therefore, the balanced expression of E1A and E1B is important to the viral life cycle. The overlapping of gene-specific regulatory elements of PAV-3 could facilitate to achieve this at the transcriptional level.

Table 4. Probes used for Northern and Southern hybridizations.

Probes	**Nucleotide position**[a]
E1A[b]	531-844
E1B[c]	1411-3077
E2A[d]	22667-23736
E3[e]	27587-29011
E4[f]	32504-33873
Southern blot in single infection[g]	934-2190
Southern blot in coinfection[h]	531-844

[a] Numbers indicate the nucleotide position (nt) relative to the left terminus of wild-type PAV-3 genome (GenBank accession No.AF083132). PAV-3 nucleotide sequences are indicated in boldface type.

[b,h] 0.3 Kb DNA fragment was generated by PCR using primers P20 (5'-CCGCAAT TG**ACATGGCGAACAGACTTC**-3', sense, nt 531-548) (SEQ ID NO: 40) and P2 (5'-**CGCGCTGATA**

TCCTCCTC-3', antisense, nt 827-844) (SEQ ID NO: 22).

[c] 1.6 Kb *Pst*I fragment released from plasmid pPAV3.XhoIRL containing the left end (nt 1-4161) of PAV-3 genome.

[d] 1.0 Kb DNA fragment was generated by PCR using primers PDBP-4 (5'-GCGTCGA**CTCAAAACAGGCTCTCAT**-3', sense, nt 22667-22684) (SEQ ID NO: 48) and PDBP-3(5'-CGGGAT**CCGGCCGCTGCTGCAGCT**-3', antisense, nt 23719-23736) (SEQ ID NO: 49).

[e] 1.4 Kb *Pst*I fragment released from plasmid pGEM32 containing KpnI/BamHI fragment (nt 26716-31064) of PAV-3 genome.

[f] 1.3 Kb *Sma*I fragment released from pPAV3.XhoIRL.

[g] 1.2 Kb *KpnI/Eco47*-3 fragment from pPAV3.XhoIRL.

Please amend paragraph no. **[0201]**, as follows:

[0201] Southern hybridization. The SpeI and KpnI digested DNAs were separated on 1.5% agarose gel and then transferred to Gene Screen Plus hybridization transfer membrane (Perkin Elmer Life Science) by high salt capillary transfer method according to the instructions of manufacturer. The 314 by DNA fragment corresponding to nt 531 and 844 was amplified by PCR

with primers P2 and PR12, labeled with ^{32}P-dCTP by the random primer method using Random Primers DNA labelling system (Invitrogen), and was used as a probe in Southern hybridization analysis. The blots were prehybridized in ULTRAhyb ultrasensitive hybridization buffer (Ambion® RNA) at 42°C for 30 min, and then ^{32}P-labeled probes were added. Hybridization was performed at 42°C overnight. After extensively washing with 0.1x SSC and 0.1% SDS, the blots were exposed to X-ray film (Kodak) without an intensifying screen. The bands in autoradiograms were scanned and their relative intensities were determined and analysed by Computing Densitometer using PhosphoImager programme (Bio-Rad), The data presented for packaging efficiency based on coinfection experiments represent the averages of three independent.

TABLE 5. PRIMERS USED IN PCR EXPERIMENTS IN EXAMPLE 5.

Primer	Sequences[a]	Nucleotide Position[b] (nt)
P1:	5'-CGTCTTCAAGGATCCTTA-3' (SEQ ID NO: 21)	sense, BamHI
P2:	5'-CGCGCTGATATCCTCCTC-3' (SEQ ID NO: 22)	(827-844) antisense
PSR32:	5'-CGGCGGGATCCTTAATTAACATCATCAATAA TATACCGCACACTTTT-3' (SEQ ID NO: 47)	(1-29)
PA1:	5'-CGGACTAGTCCGCCGCTCGGCCC-3' (SEQ ID NO: 50)	(219-233) antisense
PA2:	5'-CGGACTAGTCCCGCACAGGTGGAGAGT-3' (SEQ ID NO: 51)	(237-255) sense
PA3:	5'-CGGACTAGTCCCGCGGTACTCTCCACC-3' (SEQ ID NO: 52)	(246-264) antisense
PA4:	5'-CGGACTAGTGTGCCCTCTGGACCGGAC-3' (SEQ ID NO: 53)	(268-286) sense
PA9:	5'-CGGACTAGTCACTGAGGGGAAAAAATACA-3' (SEQ ID NO: 54)	(429-448) antisense
PA10:	5'-CGGACTAGTGTCCGCGCAGCGCCCGAGA-3' (SEQ ID NO: 55)	(455-473) sense
PA11:	5'-CGGACTAGTCTCTACTCCCTTCGGACT-3' (SEQ ID NO: 56)	(487-504) antisense

PA12:	5'-CGGACTAGTCTCTCAGCGGAACAGACCC-3' (SEQ ID NO: 57)	(508-527) sense
PL1:	5'-CGGACTAGTCTCGGCCCCGCCCCG-3' (SEQ ID NO: 58)	(212-226) antisense
PL2:	5'-CGGACTAGTAAATTCCCGCACAGGTGG-3' (SEQ ID NO: 59)	(233-250) sense
PL3:	5'-CGGACTAGTGTACTCTCCACCTGTGCG-3' (SEQ ID NO: 60)	(240-257) antisense
PL4:	5'-CGGACTAGTATTTTGTGCCCTCTGGAC-3' (SEQ ID NO: 61)	(264-281) sense
PL9:	5'-CGGACTAGTGGGGAAAAAATACACCCACA-3' (SEQ ID NO: 62)	(423-442) antisense
PL10:	5'-CGGACTAGTTATATAGTCCGCGCAGCGC-3' (SEQ ID NO: 63)	(449-467) sense
PL11:	5'-CGGACTAGTACTCCCTTCGGACTCAAG-3' (SEQ ID NO: 64)	(483-501) antisense
PL12:	5'-CGGACTAGTTTTTCTCTCAGCGGAACAG-3' (SEQ ID NO: 65)	(505-523) sense
PR1:	5'-CGGACTAGTAATTTCCGCCGCTCG-3' (SEQ ID NO: 66)	(223-237) antisense
PR2:	5'-CGGACTAGTACAGGTGGAGAGTACCGC-3' (SEQ ID NO: 67)	(243-260) sense
PR3:	5'-CGGACTAGTAAAATCCCGCGGTACTCT-3' (SEQ ID NO: 68)	(251-268) antisense
PR4:	5'-CGGACTAGTTCTGGACCGGACCTTCGC-3' (SEQ ID NO: 69)	(275-292) sense
PR9:	5'-CGGACTAGTTATATACACTGAGGGGAAAA-3' (SEQ ID NO: 70)	(435-454) antisense
PR10:	5'-CGGACTAGTGCAGCGCCCGAGAGTCACT-3' (SEQ ID NO: 71)	(461-479) sense
PR11:	5'-CGGACTAGTAAAACTCTACTCCCTTCG-3' (SEQ ID NO: 72)	(491-508) antisense
PR12:	5'-CGGACTAGTAGCGGAACAGACCCTCGAC-3' (SEQ ID NO: 73)	(514-532) sense
PM1:	5'-CGGACTAGTCGCTCGGCCCCGCC-3' (SEQ ID NO: 74)	(215-228) antisense
PM2:	5'-CGGACTAGTCACAGGTGGAGAGTACC-3' (SEQ ID NO: 75)	(242-258) sense

PM3:	5'-CGGACTAGTCGGTACTCTCCACCTGTG-3' (SEQ ID NO: 76)	(242-259) antisense
PM4:	5'-CGGACTAGTCCTCTGGACCGGACCTTC-3' (SEQ ID NO: 77)	(273-290) sense
PM5:	5'-CGGACTAGTGCCGCGGACGTGTGGTGC-3' (SEQ ID NO.78)	(312-329) antisense
PM6:	5'-CGGACTAGTACCTGACGACGGTGACAC-3' (SEQ ID NO: 79)	(342-359) sense
PM7:	5'-CGGACTAGTCCACACACGTCATCTCGG-3' (SEQ ID NO: 80)	(410-427) antisense
PM8:	5'-CGGACTAGTCTCAGTGTATATAGTCC-3' (SEQ ID NO: 81)	(442-458) sense
PM9:	5'-CGGACTAGTTGAGGGGAAAAAATACAC-3' (SEQ ID NO: 82)	(428-445) antisense
PM10:	5'-CGGACTAGTGCGCAGCGCCCGAGAGTCA-3' (SEQ ID NO: 83)	(459-477) sense
PM11:	5'-CGGACTAGTTACTCCCTTCGGACTCAA-3' (SEQ ID NO: 84)	(484-501) antisense
PM12:	5'-CGGACTAGTTCAGCGGAACAGACCCTCG-3' (SEQ ID NO: 85)	(512-530) sense

[a]The restriction endonuclease cleavage sites are underlined.

[b]Numbers indicate the nucleotide position relative to the left terminus of PAV-3 (Reddy et al., 1998) genome, PAV-3 nucleotide sequences are indicated in boldface type.